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FRDA_MOUSE
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Best Local Similarity
Thehes 5; Conservi
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CD8A_PONPY
FRDA_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP: P01732; 1CD8.
InterPro: IPR003006: Ig_MHC.
InterPro: IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SHASS PROT entry is copyright. It is produced through a collaboration between the Suis Pastitude of Bioinformatics and the BML pursation or the European Bobinformatics Institute. These are not restrictions on its de European Bobinformatics Institute. The are are not restrictions on its modified and this statement is not emposed usage by and for commercial motifies requires a license spresent (see http://www.isb-sib.ch/anounce/or.seaf on email to licensesibj=bl.ch).
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                                                                                                          3 MYFSH 7
11111
123 MYFSH 127
                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plam; PROUGA?: 19: 1.
SMART: SMOAGOS; IGv; 1.
Immunoglobulin domain; Transmembrane; Glycoprotein; T-ceil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pongo pygmaeus (Orangutan).
Elkaryota: Matazoa: Chordeta: Craniata: Vertebrata: Euteleostomi
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.APR-1993 (Hah. 25. Last sequence update)
15-UN-2002 (Ed. 41. Last annotation update)
T-cell surface glycoprotein CDB alpha chain precursor (T-lymphocyte
differentiation antigen TGA-KEV-2).
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92307742; PubMed=1612644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Isolate Jari;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel.
01-APR-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD8A_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKED BY TWO DISULFIDE BONDS. CAN ALSO PORM HOMODINESS.
SUBCELLULAN LOCATION: Type I membrane protein.
SINILARITY: BELONGS TO THE IMMUNOCIOUULIN SUPERFAMILY.
SINILARITY: CONTAINS I IMMUNOCIOBULN'LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAHLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X60223; CAA42784 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response; Signal.
1 21
22 198
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146
167
22
43
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STANDARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25, Created)
                                                                                                                                                                                                                                                                                                    22099
                                                                                                                                                                                                   33.3%; Score 5; DB I
100.0%; Pred. No. 42;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                    WW.
                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
THOUSE SUFFACE GLYCOPROTEIN CD8 ALPHA
CHAIN.
                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKT
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VV / 02
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                                                                                                                                                                                                       0,
                                                                                                                                                                                                       Indels
                                                                                                                                                                                                       0
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                       0
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RRRR OCCORDED TO

Homo sapiens (Human) CD8A OR MAL

Littman D.R., Thomas Y., Maddon

Maddon P.J.,

Chess L.,

Axel R.:

NUBI_TaxID=9605

SEQUENCE FROM N.A.

Bukaryota; Metazoa; Chordata; Craniata; Vertebratu: Mammalia; Eutheria; Primates; Catarrhini; Hominidae

CUCRTROSCOUT

COBA_MUNAM STANDARD PRT: 135 AA.

171731.06 (mai. 0.1. Crosted)

171741.06 (mai. 0.1. Lors sequence wydole)

171741.00 (mai. 0.1. Last sequence wydole)

RESULT Db 2

8 RHAHL 12 | | | | | | 51 RHAHL 55 51

Conservative

0; indels

Ç. Gaps

0

HUMAN

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Query Match
Best Local Similarity
Patches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics institute. There are we restrictions on list use by non-profit institutions as long as its content is into move modified and this statement is not removed. Usage, we and for commercial entities requires a license agreement (See http://www.isbrstb.ch/announce/or send an email to licensefish-sib.ch)
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15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                 Pfam: PE01491: Erataxin_Cyay: 1.
PRINTS: PR00394: FRATAXIN
Propom: PD005646: Frataxin_like: 1.
PROSITE: PS01344: FRATAXIN_1: 1.
PROSITE: PS5010: FRATAXIN_2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U95736; AAB67778.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- PTM: PROCESSED BY MITOCHOMINAL PROCESSING PELITIASE (MPP)
-- SINILARITY: BELONGS TO THE FRATAXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 16:345-351(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Studies of human, mouse and yeast homologues
function for frataxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Koenig M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koutníkova H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE-97385237; PubMed-9241270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Frataxin, mitochondrial precursor
                                                                                                                                                                                                                 Mitdehondrion;
                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001794; Frataxin.
InterPro: IPR002908; Frataxin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:1096879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PROBABLY INVOLVED IN IRON HOMEOSTASIS
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                                                                                                                                   41
207 AA:
                                                                                                                                                        Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDLX
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                                                                                                                                   22924 WH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chordata;
                               33.3%; Score 5; DB 1
100.0%; Pred. No. 44;
Live 0; Mismatches
                                                                                                                                   FRATAXIN.
C46FD21B44FB26A2 CHC5:
                                                                                                                                                                                       MITOCHONDRION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata: Vertebratu:
Sciurognathi: Maridae
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                                                                                   Tendin 707
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